

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- Dec 2017

B.Tech Vth Semester

COURSE CODE: 10B11BI511

MAX. MARKS:35

COURSE NAME: Structural Bioinformatics

COURSE CREDITS: 4

MAX. TIME: Two Hours

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

- Q1. What is the potential energy function and how does the internal and external parameters influence the equation? **3 marks**
- Q2. Why should one study protein electrostatics? **3 marks**
- Q3. Why do molecular dynamics simulations have the timestep in femto seconds? **3 marks**
- Q4. Describe the competitions available to check the accuracy of secondary and tertiary structure prediction? **3 marks**
- Q5. Write the algorithm for fold recognition method. **3 marks**
- Q6. What is co-evolution and what are the methods to detect co-evolved residues? **3 marks**
- Q7. Compare and contrast the first-derivative and second-derivative energy minimization methods. **3 marks**
- Q8. When does one use molecular docking? What are its advantages and disadvantages. **3 marks**
- Q9. What are the main two steps in molecular docking? **3 marks**
- Q10. Explain this statement in respect to proteins. "Nothing in Biology Makes Sense Except in the Light of Evolution". **3 marks**
- Q11. Write short notes on **5x1 mark = 5marks**
- Protein fold
 - SCOP
 - CATH
 - Structural alignment
 - Definition of domain